

A:Molecule type: DNA
A:Residues: 1-2139 <GUI>
A:Cross-references: EMBL:L03534; NID:g1850912; PID:g1850913; PIDN:AA848065.1
C:Genetics:
A:Gene: mhca
C:Superfamily: myosin heavy chain; myosin motor domain homology
F:91-780/Domain: myosin motor domain homology <M0>

Query Match 16.7%; Score 180; DB 2; Length 2139;
Best Local Similarity 27.6%; Pred. No. 0.016;
Matches 60; Conservative 52; Mismatches 77; Indels 28; Gaps 7;

QY 11 LAQEEENVLDAEFLKNEIDSVKAOISOK-----DREKRSOAIIDRLRDLERNATV 63
Db 1671 VAQEEK-----QRLESDAELEKEQLEQERTTAANAEARKKIQAELEDEYKFNLEDVYQR 1726
QY 64 ESL--QNALNKAEMLCSTLKQMKFLEQRODETKQAREAHRLCKMKMTQOIELLQSQ 121
Db 1727 EKLVAKNSEDAEI--DSLKEKKALE---DEIKITDDNNKLS-----EIDSIDRKY 1775
QY 122 RSEVEEMRDGVSQSAVEQLAVYCVSLKKEYENKEARKATGELADRLKDLVSSRSKL 181
Db 1776 NALDSKSDVSMKEKFEQDELKVKRDALETEKKNVAETMRKG---RLEKEAAEVQYRL 1831
QY 182 KTLNTELDQAKLELRSQAKDQASADOETTSLRKSSD 218
Db 1832 EALQKNLDLAQOEKAKATKDYRADGELKSLMNELD 1868

RESULT 3
T16270
hypothetical protein F35D11.11 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16270
R:Fulton, B.

submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid F35D11.

A:Reference number: 218487
A:Accession: T16270
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1827 <FUL>
A:Cross-references: EMBL:U29381; NID:g868214; PID:g868224; PIDN:AA68757.1; CESP:F35D11.1
C:Genetics:
A:Experimental source: strain Bristol N2
A:Gene: CESP:F35D11.11
A:Introns: 76/2; 131/3; 159/3; 185/3; 221/3; 253/3; 320/1; 869/3; 1133/3; 1205/2; 1250/2

Query Match 16.3%; Score 175.5; DB 2; Length 1827;
Best Local Similarity 25.3%; Pred. No. 0.024;
Matches 56; Conservative 61; Mismatches 79; Indels 31; Gaps 8;

QY 5 NKLFFDLAQEEENVLD-----AEFLKNEIDSVKAOISQDREKRDSQAIIIDTLR--- 53
Db 669 NEXYDDARKNDALLEDVATWQEKYEQLKMLEEMNRRGQEKEREADRLRLDLDKGNF 728
QY 54 ----DTLEERNATVESLONALNKAEMLCSTLKQMKFLEQRODETKQAREAHRLCKM 108
Db 729 DKLTNELKQKCVTVDSLNEEI-----SSLEQLNKSEKREKRELLRMELEQKNEM 781
QY 109 KTMQOIEL-LQSQRSVEEMIRDMGVQSAVEQLAVYCVSLKKEYENLKAARKATGELA 167
Db 782 KEERYEVKQLAEKROGVEFKEC---EARMNELTKIHEMLMEHOLKVDLHTEEV 838
QY 168 DRLKDLVSSRSKLTLNTELDQAKLELRSQAKDQASADOETTSLRK 215
Db 839 ERLKEKM---RKELEKLINEQNDGDRAEVSNERNLLESSKNNAVYELQER 884

RESULT 4

PC4035
cell-cycle-dependent 350k nuclear protein - human (fragment)

C:Species: Homo sapiens (man)
C>Date: 08-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000
C:Accession: PC4035

R:Li, Q.; Ke, Y.; Kapp, J.A.; Fertig, N.; Medsger Jr., T.A.; Joshi, H.C.
Biochem. Biophys. Res. Commun. 212, 220-228, 1995

A:Title: A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal domain suff

A:Reference number: PC4035; MUID:95336446

A:Accession: PC4035

A:Molecule type: DNA

A:Residues: 1-1017 <LIQ>
A:Cross-references: GB:U25725; NID:g818866; PIDN:AA86889.1; PID:g818867

A>Note: repeat 15-160 and 200-340
C:Comment: This protein contains a coiled-coil and a globular domain at the carboxy-t

C:Keywords: nucleoprotein; phosphoprotein
F:465/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase II) #s

F:825,826,838/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #st

F:908,909/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status

Query Match 16.3%; Score 175; DB 2; Length 1017;
Best Local Similarity 21.8%; Pred. No. 0.014;
Matches 62; Conservative 54; Mismatches 100; Indels 68; Gaps 5;

QY 1 KTIINKLFPDLAQEEN---VLDAEFLKNEIDSVKAOISQDREKRDSQAIIIDTLRDL 56
Db 56 KDKVENLERELQNEEENQELVIIDAEKSKAEVETLKQIEBMAKSLVPELDVTLNSEK 115
QY 57 EERNATVESLONALNKAEMLCSTLKQMKFLEQRO----- 91
Db 116 ENLTKQAEKQGLSELDKILSKFSKQLEKEQAEIQIKESKAVAEMLQNLKELNEAV 175
QY 92 -----DETKQAREAHRLCKMKMTQOIELLQSQRSF----- 124
Db 176 AALCGDEIMKATBQSLDPPIEEHODRNSTELKRLADEKQQLCVLQOLKESEHNA 235
QY 125 -----VEEMIRDMGVQSAVEQLAVYCVSLKKEYENLKAARKATGELADRLKDLVSSRS 179
Db 236 LKRGVENLERELIARTNOEHALLENKSGEYETLKAKIEGTQSLRGLELDVYITRS 295
QY 180 KKLTLNTELDQ-----AKLEL--RSAQKDLQASADOETTSLRKS 216
Db 296 EKEDLTNLEQKEGRISLETINSFENILQEKROEKVOKES 339

RESULT 5

T38077
hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T38077
R:Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, April 1996
A:Reference number: 221767

A:Accession: T38077

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1957 <CON>
A:Cross-references: EMBL:Z70690; PIDN:CAA94624.1; GSPDB:GN00066; SPDB:SPAC1F3.06c

A:Experimental source: strain 972h-; cosmid c1F3

C:Genetics:
A:Gene: SPDB:SPAC1F3.06c
A:Map position: 1

Query Match 15.8%; Score 169.5; DB 2; Length 1957;
Best Local Similarity 22.4%; Pred. No. 0.055;
Matches 54; Conservative 54; Mismatches 96; Indels 37; Gaps 4;

QY 15 EENVLADEFLKNEIDSVKAOISQDREKRDSQAIIIDTLRDLERNATVESLONALKAE 74
Db 1386 EDNQLATNKLKQNDHINOETIRLKEEDVLKREKESLITISLESLSNOROKESSLDAKNELE 1445

[illegible]

Query Match	15.7%	Score 169	DB 2	Length 1938
Best Local Similarity	22.6%	Pred No. 0.05%		
Matches	57	Conservative	53	Mismatches 94
				Indels 48
				Gaps 7

QY	10	DLAQEEENVLDAEFLKNEIDLSVKAQISQK-----DREKRDQSAIIDTLRDPLEE	58
		: : : : : : : : : : : : : : : : : : : :	
Db	1688	DLMOIQEDLAABERARKAQADLEKEELAEELASLSGRNTLODEKRLFEARIQILEELEE	1747
QY	59	RNAVETSLONALNKKMECLSTLKKOKKFLFLEQRDDEKQAREAHK-----	103
		: : : : : : : : : : : : : : : : : : : :	
Db	1748	EGGNMEAMSDRYRKALQAEQLSLSNELATERSTRQAQKNESARQQLERONKLEKSLQLOVEGA	1807
QY	104	LKCKKK-TMEQIIEELLQSREVEEMIRDMGQSAVEQOLAVYCVSLKEYENLKARKA	162
		: : : : : : : : : : : : : : : : : : : :	
Db	1808	VKAKLKRSTYAAALEAKLAQLEQVEQVEQAR--QAATKSLKOKDKRLKLEVLLOVEDEK-	1863
QY	163	TEGLADRLKKDLVSSRSKLTINTLELDQAKLE-----LSAQKQLQASDQ-----E	208
		: : : : : : : : : : : : : : : : : : : :	
Db	1864	---MAEQYEQAEKQKGTYYKQKLRQLEAEFEESQCNANRRKRLQGRDLDEATESNEAMGR-	1920
QY	209	ITSLRKKSDDPP	220
		: : : : :	
Db	1921	VNALKSKLGGP	1932

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RESULT 7
T42722
male-enhanced antigen-2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C:Accession: T42722
R:Kondo, M.; Sutoh, S.
DNA Seq. 7, 71-82, 1997
```

A:Title: Cloning and molecular characterization of cDNA encoding a mouse male-enhance
A:Accession: 142722
A:Reference number: Z22242; MUID:97217683
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1325 <KON>
A:Cross-references: EMBL:D78270; NID:d1096175; PID:d1020389; PIDN:BA19612.1
A:Experimental source: strain CD-1
C:Function:
C:Description: supposed to play some role for spermatogenesis
C:Keywords: leucine zipper

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Query Match 15.7%; Score 168.5; DB 2; Length 1325;
Best Local Similarity 23.8%; Pred. No. 0.04%;
Matches 69; Conservative 50; Mismatches 84; Indels 87; Gaps 12.

QY 10 DLAQEEENVLDA-EFLKNE-----LDSVKKQLSQKDREKR-----DSQAIIITLTD 54
      :|::: ||||| |::: ||::: ||::: ||::: ||
Db 590 ELQREDSQEDAIHFLQNKIYLEVALQSAKDKDELDGARRLEDTEBTSGLLEQL 649
      :|::: ||||| |::: ||::: ||::: ||::: ||

QY 55 TLEERNATIVESLQNLINKAEMLCSTLKKM-----KLELQ-----RODET-----KQ 96
      :|::: ||||| |::: ||||| |::: ||::: ||::: ||
Db 650 DLAVSNQVEHLLQEE-----TATLRKQMQVKKEBFVQGXWVAYEARRDATSKQDLINE 702
      :|::: ||||| |::: ||||| |::: ||::: ||::: ||

QY 97 ABDEARHLCKSMKMYTEQIILLQSQSEVE---EMIRMGVQSGAVEDLAYCVSLKKE 152
      :|::: ||||| |::: ||::: ||::: ||::: ||
Db 703 LKATKRRLDSEMKELRQELIKQEKKTVEHSRLQKMSLVHQMAELECHLSVQKE 762
      :|::: ||||| |::: ||::: ||::: ||::: ||

QY 153 YEN-----LKEA---RKANGELADRLKDLVSSRSKLKLTINTLDDA 191
      :|::: ||||| |::: ||||| |::: ||::: ||::: ||
Db 763 RQEMELHLSLKFDEQMALTEANETLKQIEELQOEAKKAITQEKQMKRKIGSLDTSEA 822
      :|::: ||||| |::: ||||| |::: ||::: ||::: ||

QY 192 KLELRSAQDLQSA-----DQELTSLRK-----SDPE 219
      :|::: ||||| |::: ||||| |::: ||::: ||::: ||
Db 823 QKEMKKHAYEVANSILSRQLQALASKAEATPAELNQLRAOSTGGSSDP 872
      :|::: ||||| |::: ||||| |::: ||::: ||::: ||

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RESULT 8
B33501
myosin heavy chain 2, smooth muscle - rabbit (fragment)
C:Species: *Oryctolagus cuniculus* (domestic rabbit)
C:Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 13-Aug-1999
C:Accession: B33501; A31368
R:Nagai, R.; Kuro-o, M.; Babji, P.; Periasamy, M.
J. Biol. Chem. 264, 9734-9737, 1989
A:Title: Identification of two types of smooth muscle myosin heavy chain isoforms by
A:Reference number: A33501; MUID:89255535
A:Accession: B33501
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-484 <NAG>
A:Cross-references: GB:J04833
R:Nagai, R.; Larson, D.M.; Periasamy, M.
Proc. Natl. Acad. Sci. U.S.A. 85, 1047-1051, 1988
A:Title: Characterization of a mammalian smooth muscle myosin heavy chain cDNA clone
A:Reference number: A31368; MUID:88124972
A:Accession: A31368
A:Molecule type: mRNA
A:Residues: 1-484 <NMA>
A:Cross-references: GB:J03614; NID:9165517; PIDN:AAA31406.1; PID:9165518
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: muscle; smooth muscle

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Query Match      15.6%   Score 168   DB 2:   Length 488;
Best Local Similarity 23.0%   Pred No. 0.016;
Matches 58; Conservative 52; Mismatches 94; Indels 48; Gaps 7

QY 10 DLAQEENVLDAEFLKNEIDSVKAQLSQK-----DREKPSQAIIDTLPTLEE 58
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 234 DLMQIQEDIDAAAEARRKQADLEKEELAEELASLSGRNALQDCKRLEKRIATQEELEE 293
      : : : : : : : : : : : : : : : : : : : : : : : : : : :

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QY 59 RNATVESIQNALNK---AEMLCSTLKKOMKFLERODETKOAREAHRLCKMKMTME-- 112
 Db 294 EOGNEMASDVRKATQOAEOLSNELATERSTAOGNESARQOLERÖNKLEKSLÖEMGA 353
 QY 113 -----QIELLOQSRSEVEEMITDMGVGSAVEQLAVYCVSLKKEENLKEAKA 162
 Db 354 VKSRFKSTIALEKIKIAOLEBÖVEQAEAREK---QAAAKALÖRDKKLEMLÖVEDEK- 409
 QY 163 TGEIADRLKDLVSSRSKLTINTELDOAKLE-----LRSQOKDQSDQ-----E 208
 Db 410 ---MAEQYKEQAEKGNMAVYKOLKQLEAEFEESQRINANKRKLÖRELDATESNEAMRE 466
 QY 209 ITSRLKKSDDPP 220
 Db 467 VNALSKSLRCP 478

RESULT 9
 B55094
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 02-Jun-2000
 C:Accession: B55094
 R: Hirano, T.; Mitchison, T.J.
 Cell 79, 449-458, 1994
 A:Title: A heterodimeric coiled-coil protein required for mitotic chromosome condensat
 A:Reference number: A55094; MUID:95042742
 A:Accession: B55094
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1203 <H1R>
 A:Cross-references: GB:013674; NID:g563813; PIDN:AAA64680.1; PID:g563814
 C:Superfamily: Chromosome segregation protein SWC1
 C:Keywords: chromosomal protein; DNA condensation; heterodimer

Query Match 15.6%; Score 167.5; DB 2; Length 1203;
 Best Local Similarity 24.6%; Pred. No. 0.043;
 Matches 51; Conservative 45; Mismatches 80; Indels 31; Gaps 5;
 QY 22 EFLKNELDSVKAOLSQDKREKDSOATITDRLPLEERNATVESIQNALNKAEMLCSTLK 81
 Db 721 EMKSEEMELDTKLQOSSHKQEE--LDSLKÖTIESEETLKNKTKYÖKAEKFKYLE 778
 QY 82 KOMFLE-QRODETKOARE-----EAHRLCKMKMTMEQIELLOQSRSEVEEMITD 131
 Db 779 HKMNAEERERELKEAQÖKIDTAKKADASNKKMKKEQÖEVDALV-----ELEELKRE 833
 QY 132 MGVGSAVEQLAVYCVSLKKEENLKEAKATGELADRLKDLVSSRSKLTINTELDOA 191
 Db 834 Q-----TTYKQÖIEIVDEAMKAYQEQADSMASEVSKNKEAVYKQDELAKQ 879
 QY 192 KLELRSQOKDQSDQSDPP 218
 Db 880 KEITMGHDKETKTSSEKGLKENND 906

RESULT 10
 A36014
 C:Species: Drosophila melanogaster
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
 C:Accession: A36014; B36014
 R:Ketchum, A.S.; Stewart, C.T.; Stewart, M.; Kiehart, D.P.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6316-6320, 1990
 A:Title: Complete sequence of the Drosophila nonmuscle myosin heavy-chain transcript: c
 A:Reference number: A36014; MUID:90349606
 A:Accession: A36014
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-2017 <KEY>
 A:Cross-references: GB:M35012

C:Genetics:
 A:Gene: FlyBase:zip
 A:Cross-references: FlyBase:FBgn0005634
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: actin binding; alternative splicing; ATP; coiled coil; hydrolase; methyl
 F:1-2017/Product: myosin heavy chain, form I #status predicted <MA1>
 F:46-2017/Product: myosin heavy chain, form II #status predicted <MA2>
 F:135-815/Domain: myosin motor domain homology <MMOT>
 F:225-232/Region: nucleotide-binding motif A (P-loop)
 F:568-631/Region: actin binding #status predicted
 F:705-727/Region: actin binding #status predicted
 F:888-2017/Domain: coiled coil #status predicted <CO1>
 F:1329-2017/Region: light meromyosin
 F:176/Modified site: N6,N6,N6-trimethyllysine (lys) #status predicted
 F:231/Binding site: ATP (lys) #status predicted
 F:745,755/Active site: Cys #status predicted

Query Match 15.4%; Score 166; DB 1; Length 2017;
 Best Local Similarity 25.2%; Pred. No. 0.089;
 Matches 61; Conservative 47; Mismatches 96; Indels 38; Gaps 8;
 QY 1 KTIINKLFFDLAÖEENVLDAE--FLKNEELDSVKAOLSQDKREKDSQ-----AI 48
 Db 1263 KTVLEK-----AKGTLEENADLATELRSVSSHQENRRKQAESQIAELQVKLAE 1314
 QY 49 IDTLRLPLEER-----NATVESIQNALNKAEMLCSTLKKOMKFLERODETKOAREAHRL 103
 Db 1315 IERARSELÖEKCCTKLOQEAENITNÖLEAEIKASAAVKSANMSQULTQÖÖLLEETRQ 1374
 QY 104 ---LKCKMKTMEQIELLOQSRSEVEEMITDMGVGSAVEQLAVYCVSLKKEENLKEAR 160
 Db 1375 KLGLSSKRLQÖSEKALQÖLEEDDEAKRNY---EKLAEVYTTQÖEIKKAEQADLA 1431
 QY 161 KATGELADRLKDLVSSRSKLTINTELDOAKLELRSQOKDQSDPP 218
 Db 1432 KELEEGKRLNKDIEALRQVKELIAÖNDRDKSKRKQÖSELEDATIELBAQRTKYLE 1491
 QY 214 KK 215
 Db 1492 KK 1493

RESULT 11
 S61477
 C:Species: Drosophila melanogaster
 C:Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 02-Feb-2001
 C:Accession: S61477; S65349
 R:Mansfield, S.G.; Al-Shirawi, D.Y.; Ketchum, A.S.; Newbern, E.C.; Kiehart, D.P.
 J. Mol. Biol. 255, 98-109, 1996
 A:Title: Molecular organization and alternative splicing in zipper, the gene that enc
 A:Reference number: S61477; MUID:9614835
 A:Accession: S61477
 A:Molecule type: DNA
 A:Residues: 1-2057 <MAN>
 A:Cross-references: EMBL:U05816
 R:Mansfield, S.G.; Al-Shirawi, D.Y.; Ketchum, A.S.; Newbern, E.C.; Kiehart, D.P.
 Submitted to the EMBL data library, September 1995
 A:Reference number: S65349
 A:Accession: S65349
 A:Molecule type: DNA
 A:Residues: 1-1908, 'NL', 1911-2057 <MAN>
 A:Cross-references: EMBL:U05816; NID:g1141789; PIDN:AAB09049.1; PID:g1572481
 C:Genetics:
 A:Gene: zip
 A:Cross-references: FlyBase:FBgn0005634
 A:Introns: 10/3; 90/3; 162/3; 215/1; 255/3; 263/3; 303/3; 334/3; 1248/1; 1349/3; 1526
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: alternative splicing; ATP; nucleotide binding; P-loop
 F:135-855/Domain: myosin motor domain homology <MMOT>
 F:225-232/Region: nucleotide-binding motif A (P-loop)

Query Match 15.4%; Score 166; DB 2; Length 2057;

Best Local Similarity 25.2%; Pred. No. 0.09; Mismatches 96; Indels 38; Gaps 8;

Matches 61; Conservative 47; Mismatches 96; Indels 38; Gaps 8;

QY 1 KTIINKLFFDLAEEENVLDAAEFLKNELDVSKAQLSOKDREKRSQAIIPTLRDTLEERN 60
 DB 1303 KTVLEK-----AKGTLEENADLATELRVSNSSHQENDRRKQKQESQALQVLAEL 1354
 QY 49 IDTLRDTLEER-----NATVESLONALKAEMLCSTLKQKMFLEQRODETKQAREAHN- 103
 DB 1355 IERRASSELQKCTKQLQQAENITNQLEAEELKASAAVKSASNMESQULEAQOQLLEETRQ 1414
 QY 104 ---LCKCKMTMEQIETLLQSORSEVEEMIRDMGVGQSAVOLAVYCVSLKKEYENLKEAR 160
 DB 1415 KLGLSSLRQIESKEKALQDLEEDDEAKRNY---ERKLEAVTQMQEIKKKAEDDLA 1471
 QY 161 KANGELADRLKKDLVSSRSKLTFL--NTELDQAKLELRSAQND---LOSADQETSLR 213
 DB 1472 KELEEGKKRLNKDIEALERQVKELIAQNDRLDKSKKIKQSELDQATELEAQRTKVELE 1531
 QY 214 KK 215
 DB 1532 KK 1533

RESULT 12

T47237
 myosin II heavy chain [imported] - Naegleria fowleri (fragment)
 C:Species: Naegleria fowleri
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C:Accession: T47237
 R:Shaw, D.R.; Sullivan, P.K.; Marciano-Cabral, F.; Ennis, H.L.
 submitted to the EMBL Data Library, December 1995
 A:Description: Codon usage in Naegleria fowleri.
 A:Reference number: 224413
 A:Accession: T47237
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-746 <SHA>
 A:Cross-references: EMBL:U43192; PIDN:AAB01786.1
 A:Experimental source: strain LEE mp; cell type amoeba

Query Match 15.3%; Score 164.5; DB 2; Length 746;
 Best Local Similarity 22.7%; Pred. No. 0.039;
 Matches 57; Conservative 57; Mismatches 104; Indels 33; Gaps 4;

QY 1 KTIINKLFFDLAEEENVLDAAEFLKNELDVSKAQLSOKDREKRSQAIIPTLRDTLEERN 60
 DB 167 KQLONELQNETNTNQKKSENERLQRELEEKRLSDKQNESTLSDKVSLEDKITELT 226
 QY 61 ATVESLONALKAEMLCSTLKQKMFLEQRODETKQA-REBAHRLCKMKMTMEQIETLLQ 119
 DB 227 ALLETTERSSKTDIDDKRSKDKKQEVKRLAQQLQETQALKGCTQKNDADNRVKQLESELQ 286
 QY 120 SQRESEVEEMIRDMG-----VGQSAVEQIAVYCVSLKKEYENLKEARKATGE 165
 DB 287 GVKSESRRLNKDLNNTSGDMNGELKRLQLESDSNVLAKLAETQKLOKPLSDHHGDEETEE 346
 QY 166 LADLKLDIVSSRSKLT-----KTLNTELDQAKLELRSAQND---Q 207
 DB 347 QLDLRLKQLOELTIRLSDANOKTQOEAAKRONLESENRLKSEVSRRLQDNLQENRRLKQ 406
 QY 208 EITSLRRKSSD 218
 DB 407 EMERVOSESEN 417

RESULT 13
 F96673
 hypothetical protein F13011.30 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: F96673

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 ansen, N.F.; Hughes, B.; Huzar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marzia
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719
 A:Accession: F96673
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1313 <STO>
 A:Cross-references: GB:AE005173; NID:95042434; PIDN:AAD38273.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F13011.30
 A:Map position: 1

Query Match 15.2%; Score 163; DB 2; Length 1313;
 Best Local Similarity 22.8%; Pred. No. 0.083;
 Matches 67; Conservative 52; Mismatches 81; Indels 94; Gaps 9;

QY 12 AQEEENVLD-----AEFLKNELDVSKAQL-SQKDREKRSQAIIPTLRDTLEERNATVES 65
 DB 182 AEEATKIAETIAEKAETELASLGLKALSLKSEKEAIEGNEIVSKLK-----SEIEL 234
 QY 66 LQNALNKAEMLCSTLKQKMFLEQRODETKQAR-----EEL 101
 DB 235 LRGELEKVSITLESLLKQEGVLEQKLVLEAKAASCTSVSEVKKYHELEKEYES 294
 QY 102 HRLCK-----MKT-----EQLLEL--LOSQRESEVEEMIRDM 132
 DB 295 NRSKSSASESMESVMKQALDELINHLHETKSDMAQKRIELEETIEAQRTDLEEVGRV 354
 QY 133 VGQSAVEQIAVYCVSLKKEYE-----NLKARATGELAD----- 168
 DB 355 CIAKEEASKLENIWESIKSELEISQEEKTRALDNEKAATNIONLIDQRTELSIELECRK 414
 QY 169 -----RLKKDLVSSRSKLTINTELDQAKLELRSAQNDQESQALQVLAEL 218
 DB 415 VEEKSKDKMESTLTLAQEASTESSEKATPLVCQELKNCESOVDSLKASKE 468

RESULT 14

S67593
 transport protein USO1 - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein D2552; protein YDL058w
 C:Species: Saccharomyces cerevisiae
 C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 21-Jul-2000
 C:Accession: S67593; A38455; S30782
 R:Bioecker, H.; Brandt, P.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S67587
 A:Accession: S67593
 A:Molecule type: DNA
 A:Residues: 1-1790 <BLQ>
 A:Cross-references: EMBL:T47106; NID:91431058; PID:e253003; PID:g1431059; MIPS:YDL058
 A:Experimental source: strain S288C
 R:Nakajima, H.; Hirata, A.; Ogawa, Y.; Yonehara, T.; Yoda, K.; Yamasaki, M.
 J. Cell Biol. 113, 245-260, 1991
 A:Title: A cytoskeleton-related gene, USO1, is required for intracellular protein tra
 A:Reference number: A38455; MUID:21185402
 A:Accession: A38455
 A:Molecule type: DNA
 A:Residues: 1-389, 'TA', 392-724, 'S', 726-1790 <NKA>
 A:Cross-references: GB:X54378; NID:94777; PIDN:CAA38253.1; PID:94778
 A:Note: the authors translated the codon ACP for residue 768 as Ile

R:Hostetter, M.K.; Herman, D.J.; Bendel, C.M.; McClellan, M.; Tao, N.; Kendrick, K.E.
submitted to the EMBL Data Library, February 1993
A:Description: An integrin analogue in Saccharomyces cerevisiae.

A:Reference number: S30782

A:Accession: S30782

A:Molecule type: DNA

A:Residues: 71-846, 'E', 848-923, 'K', 925-1252, 'I', 1254-1318, 'V', 1320-1460, 'S', 1462-1580, 'S'

A:Cross-references: EMBL:103188

C:Genetics:

A:Gene: SGD:USO1; INT1

A:Cross-references: SGD:S0002216; MIPS:YDL058w

A:Map position: 4L

C:Keywords: coiled coil; transmembrane protein

F:326-342/Domain: transmembrane #status predicted <TM1>

F:394-410/Domain: transmembrane #status predicted <TM2>

F:617-633/Domain: transmembrane #status predicted <TM3>

Query Match 15.2%; Score 163; DB 2; Length 1790;

Best Local Similarity 23.7%; Pred. No. 0.11;

Matches 51; Conservative 57; Mismatches 77; Indels 30; Gaps 7;

Qy 10 DLAGEENVLDAEFLKNELDVSKAQLSOKDKREKRSQAIIIDTLRDLTEERNATVESLQNA 69

Db 1424 ELLEKQNTIKS--LQDEI-----LSYKDKITRNDKELSLERNKRD---LESLKEQ 1471

Qy 70 LNKAEMLCSTLKQMKFEORODETKQAREAHRLCKMKTMEOTELLQSORSEVEEMI 129

Db 1472 LRAQESAKAYEGLKTEESSKKALEKSKEM-----MKLESTIESNETELKSSM 1525

Qy 130 RDMGVGSAVBOQLAVYCVSLKREYENLKEARKANGELADRL--KKDLVSSRSKLK--T 183

Db 1526 ETIRKSDLEKQ-----SKKSAEDIKNLQHEKSDLSRINESEKDIELKSKLRIRAK 1579

Qy 184 LNTLEDAKLELRSAQKLDQSAQDOEITSLRKKSD 218

Db 1580 SGSELETYKQELNNAQEKIRINAEENTVLKSKLELD 1614

RESULT 15

A26655

myosin heavy chain [similarity] - slime mold (Dictyostelium discoideum)

N:Contains: myosin ATPase (EC 3.6.1.33)

C:Species: Dictyostelium discoideum

C>Date: 05-Oct-1988 #sequence.revision 05-Oct-1988 #text.change 02-Feb-2001

C:Accession: A26655; A24728; S00250

R:Warrick, H.M.; DeLozanne, A.; Leinwand, L.A.; Spudich, J.A.

Proc. Natl. Acad. Sci. U.S.A. 83, 9433-9437, 1986

A:Title: Conserved protein domains in a myosin heavy chain gene from Dictyostelium disc

A:Reference number: A26655; MUID:87092266

A:Accession: A26655

A:Molecule type: DNA

A:Residues: 1-2116 <MAR>

A:Cross-references: GB:M14628; GB:M11938; NID:g167834; PIDN:AAA33227.1; PID:g167835

R:DeLozanne, A.; Lewis, M.; Spudich, J.A.; Leinwand, L.A.

Proc. Natl. Acad. Sci. U.S.A. 82, 6807-6810, 1985

A:Reference number: A24728; MUID:86016788

A:Accession: A24728

A:Molecule type: mRNA

A:Residues: 2035-2116

R:Wagle, G.; Noegel, A.; Scheel, J.; Gerisch, G.

FEBS Lett. 227, 71-75, 1988

A:Title: Phosphorylation of theonline residues on cloned fragments of the Dictyostelium

A:Reference number: S00250; MUID:88112226

A:Accession: S00250

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1734-1893 <MAG>

C:Comment: The rod domain is highly periodic, containing a pattern of 7-residue repeats

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: actin binding; ATP; coiled coil; hydrolase; nucleotide binding; P-loop; phos

F:1-818/Domain: globular head <HEB>

F:89-747/Domain: myosin motor domain homology <MMOT>

F:179-186/Region: nucleotide-binding motif A (P-loop)

F:819-2116/Domain: alpha-helical rod <ROD>

Query Match 15.1%; Score 162.5; DB 2; Length 2116;

Best Local Similarity 25.0%; Pred. No. 0.15;

Matches 67; Conservative 52; Mismatches 86; Indels 63; Gaps 11;

Qy 5 NKLFFDLAQEEENVLDAEFLKNELDVSKAQLSOKDKREKRSQAIIIDTLRDLTEERN 60

Db 852 DKLEKSLKDTQSNVLDLQRLKAKEETLKANYDSKDALQAKRELETRVEEMSELEDEK 911

Qy 61 ATVESLQ-----ALNKAEMLCSTLKQMKFEORODETKQAREAHRLCK 106

Db 912 LALENLQNKQKSVKEKVRADLEELQEBQKLNLTLEKLKKYEELEEKRVNDG----- 965

Qy 107 MKKTMEOTELLQSORSEVEEMI-----RDMGV-----GSAVBOQLAVYCVS---- 148

Db 966 QSDTISRLEKIKDELQKVEELTFSESEKDKGVLEKTRVRLQSELDLTVRLDSETKD 1025

Qy 149 -----LKKREYENLKEARKA-TGELADRLKKDLVSSRSKLTLNTELDQ-----AKL 193

Db 1026 KSELLRQKKLEELKQYQALAEATAKLQAE--AAKKLQGEYTELNEKFNSEVTARS 1083

Qy 194 ELRSQKQDLQS---ADQETSLRKKSD 217

Db 1084 NVEKSKTKLESQLVAVNNLEDEKKNRD 1111

RESULT 16

A40997

myosin heavy chain, striated adductor muscle - scallop (Aequipecten irradians)

N:Contains: myosin ATPase (EC 3.6.1.32)

C:Species: Aequipecten irradians

C>Date: 31-Dec-1993 #sequence.revision 31-Dec-1993 #text.change 19-Jan-2001

C:Accession: A40997; S13557

R:Nyitra, L.; Goodwin, E.B.; Szent-Gyorgyi, A.G.

J. Biol. Chem. 266, 18469-18476, 1991

A:Title: Complete primary structure of a scalllop striated muscle myosin heavy chain.

A:Reference number: A40997; MUID:92011595

A:Accession: A40997

A:Molecule type: mRNA

A:Residues: 1-1938 <NYI>

A:Cross-references: GB:V55714; NID:95611; PIDN:CAA39247.1; PID:95612

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: actin binding; ATP; coiled coil; hydrolase; muscle contraction; nucleotide

F:86-763/Domain: myosin motor domain homology <MMOT>

F:116-183/Region: nucleotide-binding motif A (P-loop)

F:547-586/Region: actin binding #status predicted

F:653-675/Region: actin binding #status predicted

F:836-1938/Domain: coiled coil #status predicted <COI>

F:836-1276/Region: S2

F:1277-1938/Region: light meromyosin

F:182/Binding site: ATP (Lys) #status predicted

F:693/703/Active site: Cys #status predicted

Query Match 15.1%; Score 162; DB 1; Length 1938;

Best Local Similarity 24.5%; Pred. No. 0.14;

Matches 73; Conservative 50; Mismatches 89; Indels 86; Gaps 12;

Qy 1 KTIINKLFFD-----LQAEENVLDAEFLKNELDVSKAQLSOKDKREKRSQAIIIDTLRDLTEERN 38

Db 904 KLINQKQDFESQIKLEBERLDEDAADLEGIKKKHADVANANKKQIGLENTLQKAEQ 963

Qy 39 DREKRDSQAIIIDTL-----RDTLEERN-ATVESLQ-----NALNKA 74

Db 964 DKAKKRDQ--ISTLQGEISODDEHIGLKNKREKKALEANKKTSLSQAEEDKCNHLNK-- 1019

Qy 75 MLCSTLKQMKFEORODETKQAREAHRLCKK-----TMDEILLQSORSEVEEMI 129

Db 1020 -LNAKLEQALDELNDLNERKKYGVDEAKKRVQDLKSTQENVEDLERYKR-ELRENV 1077

QY 130 R-----DMGQSAVEQLAVYCVSLKKEYNLEKREKATGELADRLKDLVSSR 178
 Db 1078 RRKEAEISSLNLSKLEDEQNLVSQLQRIKELQARIELEELAEENARNAKVEKQRAELN 1137
 QY 179 SKAKTLNTELDQA-----KLELRSAQKDLQSA---DOETISLRKSSD 218
 Db 1138 RELEELGERLDEAGATSAQIQLNKKRELELLKIRRLDEEASLQHEAQISALRKKHOD 1195
 RESULT 17
 152860
 smooth muscle myosin heavy chain isoform SM2 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
 C:Accession: I52860
 R:Alkawa, M.; Sivam, P.N.; Kuro-o, M.; Kimura, K.; Nakahara, K.; Takewaki, S.; Ueda, M.;
 Cite. Res. 73, 1000-1012, 1993
 A:Title: Human smooth muscle myosin heavy chain isoforms as molecular markers for vascul
 A:Reference number: I52860; MUID:94037315
 A:Accession: I52860
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-296 <RES>
 A:Cross-references: GB:S67238; NID:q452982; PIDN:AA828950.1; PID:q452983
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: ATP; smooth muscle

Query Match 15.0%; Score 161; DB 2; Length 296;
 Best Local Similarity 23.8%; Pred. No. 0.023;
 Matches 60; Conservative 52; Mismatches 92; Indels 48; Gaps 9;

QY 10 DLAOEENVLDAEFLKNELDVKAQLSOK-----DREKRSQATIIDRLPTLEE 58
 Db 46 DLQLOEDLLAAERARQKQLEKELEAEELASSLGNALQDERKRLAEATIAQLEEELE 105
 QY 59 RNATVESIQALNK---AEMLC-----STLKQKMFLEORODETKQAREAHRL--- 104
 Db 106 EOGNEMASDRVRKATQQAQQLSMLATERTTQKNESARQQLERQKELRSKHEHEGA 165
 QY 105 -KCKMK-TMQOIELLOSQSEVEEMTRDMGVGQSAVEQLAVYCVSLKKEYNLEKRA 162
 Db 166 VKSKFKSTIALAEAKIAQLEQVEQEARERK---QAATKSLKOKDKKLKEILLQVEDERK- 221
 QY 163 TGEIADLKDKDIVSSRSKTLTNTLTDQAKLE-----LRSAQKDLQSDQ-----E 208
 Db 222 ---MAEQYKQDAEKGNAGVQKLRQLEAEESORINANRRKLQRLDEATESENEMAGRE 278
 QY 209 ITSIRKKSDDPP 220
 Db 279 VNALSKSLRGP 290

RESULT 18
 JH0720
 tanabin - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 21-Jul-2000
 C:Accession: JH0720
 R:Hemmati-Briyvanlou, A.; Mann, R.W.; Harland, R.M.
 Neuron 9, 417-428, 1992
 A:Title: A protein expressed in the growth cones of embryonic vertebrate neurons defines
 A:Reference number: JH0720; MUID:92338961
 A:Accession: JH0720
 A:Molecule type: mRNA
 A:Residues: 1-1744 <HEM>
 A:Cross-references: GB:M9387; NID:q214816; PIDN:AAA49966.1; PID:q214817
 A:Experimental source: tadpole head
 C:Keywords: Intermediate filament

Query Match 14.9%; Score 160.5; DB 2; Length 1744;
 Best Local Similarity 24.3%; Pred. No. 0.15;

Matches 57; Conservative 58; Mismatches 71; Indels 49; Gaps 8;
 QY 12 AOEENVLDAEFLKNELDVKAQLSOKDREKRSQATIIDRLPTLEERNATVESIQALN 71
 Db 33 ALEEN---ELRKELHSLRSKSEKCKKHEEM-KLRDALDGH-----REMY 80
 QY 72 KAEMLCTLKQKMFLEORODETKQAREAHRLKCKMTMQOIELLOSQSEVEEMTRDMGVGQSAVEQLAVYCVSLKKEYNLEKRA-----TGELADR 169
 Db 81 QAEMVADSIYELEIEFYKQRLERKQAREDA-----KELSESKKLEEFRAQIMLKERL 135
 QY 123 ---SEVEEMTRDMGVGQSAVEQLAVYCVSLKKEYNLEKRA-----TGELADR 169
 Db 136 GQLEAELEDILRDHEBEKALME---EIASFSQRLNFVAPVAPFVEVDYARKLSET 192
 QY 170 LKQDLVSSRSKTLTNTLTDQAKLELRSAQKDLQSDQ-----LQSDQETISLRKSSD 217
 Db 193 WQAVEEYKQSEVSLVLAGLSESKENIRKYLENNKRLQLQSDKELVSLKMKRE 247

RESULT 19
 A59294
 skeletal myosin - nematode (Onchocerca volvulus)
 N:Alternate names: major body wall myosin
 C:Species: Onchocerca volvulus
 C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 08-Sep-2000
 C:Accession: A59294
 R:Werner, C.; Rajan, T.V.
 Mol. Biochem. Parasitol. 50, 255-260, 1992
 A:Title: Comparison of the body wall myosin heavy chain sequences from Onchocerca vol
 A:Reference number: A59294; MUID:92158005
 A:Accession: A59294
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-1957 <WER>
 A:Cross-references: GB:M74066; NID:q159892; PIDN:AAA29420.1; PID:q159893
 A:Experimental source: sex female
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 F:87-773/Domain: myosin motor domain homology <MMO>

Query Match 14.9%; Score 160.5; DB 2; Length 1957;
 Best Local Similarity 21.5%; Pred. No. 0.17;
 Matches 59; Conservative 56; Mismatches 83; Indels 77; Gaps 10;

QY 10 DLAOEENVLDAEFLKNELDVKAQLSOKDREKRSQATIIDRLPTLEERNATVESL-- 66
 Db 942 DLSRSKKIENDVYENLKKSIAELETRLOKTDADQKQSEDOIRTLQDEMQQODENIAKLNK 1001
 QY 67 ---QNALRKAEW-----LCSTLKQKMFLEORODETKQAREAHRL--- 103
 Db 1002 EKKHQEINRKLMDLOVEDKGNYSKLGKLEQSLDLELDNLERKRRNLEKOKRK 1061
 QY 104 ---LCKMKMTMQOIELLOSQSEVEEMTRDMGVGQSAVEQLAVYCVSLKKEYNLEKRA-----TGELADR 169
 Db 1062 IGGELKVAQENMEIE---RQRHEISNLKKEKTEQAATARLEQODLVGKLKQVNE 1117
 QY 142 LAYYCVSLKKEYNLEKARAKATGELADRLKDLVSSRSKTKTLNTELDQ----- 190
 Db 1118 TQNKITTELEELENEROSRSK---AERAKSDL---QRELEELGDRLDEAGGATAQAVEV 1170
 QY 191 ---AKLELRSAQKDLQSA---DOETISLRKSSD 218
 Db 1171 NKKRELAELARLRLDEANMHNENQLAIRKKHND 1205

RESULT 20
 MMKN
 myosin heavy chain B [similarity] - Caenorhabditis elegans
 N:Contains: myosin ATPase (EC 3.6.1.32)
 C:Species: Caenorhabditis elegans
 C:Date: 13-Jun-1983 #sequence_revision 19-May-2000 #text_change 19-Jan-2001
 C:Accession: T20770; T21629; A93958; A93287; A21074; A02992
 R:Kershaw, J.

Db 1190 ROKHSQAEELAELEQTRKRVANLEKAKOTLENERGELANEVKVLLQGRDSEHKRRV 1249
 Oy 126 EEMIRDMGV-----GOSAEVOLAVYCVSLKKEYENLEKARKATGELADRLKKDLVSSRSKL 181
 Db 1250 EAQLOELQVKNFEGRRRTTELADKATKLOVELDNTGLSSDSKSSKLTRDFSALESOL 1309
 Oy 182 K-----TLNTELDQAKLELRSQKDLQSDAQE-----ITSL 212
 Db 1310 QDTQELLQEENRQKRLSTKLQVDEKKNPFQLEEEBEKKNHLEKQIATLHQAQVDM 1369
 Oy 213 RKSSD 218
 Db 1370 KKKMED 1375

RESULT 25
 H69378
 conserved hypothetical protein AF1032 - Archaeoglobus fulgidus
 C:Species: Archaeoglobus fulgidus
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
 C:Accession: H69378
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 , Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Atliach, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea
 A:Reference number: A69250; MUID:96049343
 A:Accession: H69378
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-886 <KLE>
 A:Cross-references: GB:AF001032; GB:AF000782; NID:92689355; PIDN:AA90211.1; PID:9264956
 C:Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032

Query Match 14.76; Score 157.5; DB 2; Length 886;
 Best Local Similarity 22.38; Pred. No. 0.11;
 Matches 56; Conservative 71; Mismatches 83; Indels 41; Gaps 9;

Oy 1 KTIINKLFDDLAQEEENVLDAEFLKNELDVKAQ-----LSQKDR-KRDSQAII 49
 Db 207 ESLRKKESEEVNLSRKELEHKSRLSEKSSVLOEVRGLEELKRELOKLEEV 266
 Oy 50 DTLRDTLEERNATVESLONALNK---AEMLCSTLKKKKPFLEOR-----ODETK 95
 Db 267 ERIED-LEKKAKEVKELEKPKAEKRSILEKLSSEIMQALRDVEKREGDLTREAAQIQAOQK 325
 Oy 96 QAREBAHRLCKMKMTQEOI-----LLLOSQSEVEEMIRDMGVGOSAVEOLAVY 145
 Db 326 KAEEDNSKLEETIKRIEELERLEKFSHRLERLTKPKMRM---QGI-KAKLEKNLT 381
 Oy 146 CYSLSKKEEENLEKARKATGELADRLKKDLVSSRSKLTLNTELDQAKLELRSQKDLQSA 205
 Db 382 PDKEKMDLSSKAKEEKEITEKLK-LIAKSSLSKTRGAOLKKAVEELKSAERTCPVC 440
 Oy 206 DOETSLRKS 216
 Db 441 GRELDDEHRKN 451

RESULT 26
 184737
 kinesin heavy chain - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
 C:Accession: 184737
 R:Gudkov, A.V.; Kazarov, A.R.; Zhimazaya, R.; Axenovloch, S.; Mazo, I.A.; Roninson, I.B.
 Proc. Natl. Acad. Sci. U.S.A. 91, 3744-3748, 1994
 A:Title: Cloning mammalian genes by expression selection of genetic suppressor elements;
 A:Reference number: 149673; MUID:94224818
 A:Accession: 184737

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-881 <RES>
 A:Cross-references: GB:I27153; NID:9468354; PIDN:AAA20133.1; PID:9468355
 C:Genetics:
 A:Gene: Khcs
 C:Superfamily: kinesin heavy chain; kinesin motor domain homology
 F:9-331/Domain: kinesin motor domain homology <KMT>

Query Match 14.68; Score 157; DB 2; Length 881;
 Best Local Similarity 24.28; Pred. No. 0.12;
 Matches 57; Conservative 48; Mismatches 93; Indels 38; Gaps 6;
 Oy 10 DLAOEE-ENVDAEFLKNELDVSKAQLSQKREKDSQAIIIDTLRDTLEERNATVESLON 68
 Db 482 DASKEVEKVLQA-----LEELAVNTQKQSEVEDKTKREYLLSDENQSAIATLSDA 535
 Oy 69 ALNK-----AEMLCSTLK-----KKMFLEORODETKQAREBAH 102
 Db 536 ELQKKEKENTNQKRAAMASLLKDLAELGAVGNNDVKQPEGTGMIDEFTVRLYIS 595
 Oy 103 RLCKMKTM---EOIELLOSQSEVEEMIRDMGVGOSAVEOLAVYCVSLKKEYENLE 158
 Db 596 KMKSEVTKVRKQLESTQTESNKKMEENEKELAACOLRSOHEAKIKSLTEYLVANVEQ 655
 Oy 159 ARKATGELADRLKKDLVSSRSKLTLNTELDQAKLELRSQKDLQSDAQEITSLRK 214
 Db 656 KKRQLESVDSIGELVLRQAEKVEHEKEHLN-KVQTANEVQAVQEQIQSHRE 710

RESULT 27
 S06117
 myosin heavy chain, nonmuscle (clone lambda-FMHC) - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Jun-2000
 C:Accession: S06117
 R:Katsuragawa, Y.; Yanagisawa, M.; Inoue, A.; Masaki, T.
 Eur. J. Biochem. 184, 611-616, 1989
 A:Title: Two distinct nonmuscle myosin-heavy-chain mRNAs are differentially expressed
 S:Reference number: S06116; MUID:90032648
 A:Accession: S06117
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-924 <KAT>
 A:Cross-references: GB:X17590
 A:Note: this translation is not annotated in GenBank entry G6MHCFC, release 114
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 F:1-303/Domain: myosin motor domain homology (fragment) <KMT>

Query Match 14.68; Score 157; DB 2; Length 924;
 Best Local Similarity 21.38; Pred. No. 0.12;
 Matches 65; Conservative 58; Mismatches 92; Indels 90; Gaps 10;
 Oy 4 INKLFFDLAQEEENV-----LDAEF--LKNELDSVKAQLSQK 38
 Db 610 ITELKIQAKKEEELQALANGDEAVQKNALVIRLQALQVLEQDLESEKASRKA 669
 Oy 39 DREKRDQAIIIDTLRDTLEERNATVESLONALNKAEMLCSTLK-----QMKFL 87
 Db 670 EKQKRDLSSELEALKTELDITDTTAAQOELRTKREGQVVALKAIIBETKKNHEAOIOEI 729
 Oy 88 EQRO-----DETKQAREBAHRLK-----CKMTMEDIELLOSQ--- 122
 Db 730 RQRNATALEELSEDLQAKRKANLEKKNQGLSDNKLQACEVAVLVQVKAESHKRKL 789
 Oy 123 -SEVEEMIRDMGVGOSAVEOLAVYCVSLKKEYEN-----LKEARRA----- 162
 Db 790 DAQVDELAKTATGGERLRLVAELKANKLQNELDVVSSLSLEAEKKGKIFAKDAASLESOL 849
 Oy 163 --TGEADRLKKDLVSSRSKLTLNTE--LDQAKLELRSQKDLQ-----SADQETSLR 213

Db 850 QDPQELLOEETROKLNLSRIROLEEKNMLQEQEEERARRNLEKOMLALOQLAEAK 909
QY 214 KKSDD 218
Db 910 KKVD 914

RESULT 28
T14867
Interaptin - slime mold (Dictyostelium discoideum)

C:Species: Dictyostelium discoideum
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C:Accession: T14867
R:Rivero, F.J.; Kuspa, A.; Brokamp, R.; Matzner, M.; Noegel, A.A.
J. Cell Biol. 142, 735-750, 1998

A:Title: Interaptin, an actin-binding protein of the alpha-actinin superfamily in Dictyos-

ts.
A:Reference number: Z18248; MUID:98365468

A:Accession: T14867

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1738 <R1Y>

A:Cross-references: EMBL:AF057019; NID:g3549260; PID:g3549261; PIDN:AAC34582.1

C:Genetics:

A:Gene: abpd

A:Introns: 173/2; 1680/1

Query Match 14.6%; Score 157; DB 2; Length 1738;
Best Local Similarity 26.7%; Pred. No. 0.24;
Matches 56; Conservative 39; Mismatches 85; Indels 30; Gaps 7;

QY 20 DAELFKNELDSVKAQLSQKREKRDQAIIITLRLTLEERNATVESLQNALNKAEMLCST 79
Db 1296 DLNQLKQENQEKQKQSEKQKQSLQSDLNQDNDQIKRN---EKLK---EKEEQL--- 1346
QY 80 LKKOMKRLFEORODETKAREREAHRLKCKMTMEQ---TELLLOSREYEEMIRMGVY 135
Db 1347 LKLOQDPNDQSQQLKQLEKLEKENQLOQKQENQINQNLQSQSQNEITIQQLKDLK 1406
QY 136 QSAVEQLAVYCVSLKKEYNELKARKATGELADRLK-----DIVSSRSKLTNTL 188
Db 1407 QQQQEQ-----QENNEKEKEIERLQEI-EQLKQEQEIDQSELNKEIKIQTQOEF 1456
QY 189 DQAKLELSAQKDLQSDAQDQITSLRKSDD 218
Db 1457 DQLSHNRSKDQLHLQQLQELQDLQKQSFDD 1486

RESULT 29
B43402
myosin heavy chain-B, neuronal - chicken

N:Contains: myosin ATPase (EC 3.6.1.32)

C:Species: Gallus gallus (chicken)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001

C:Accession: B43402; A43402

R:Takahashi, M.; Kawamoto, S.; Adelstein, R.S.
J. Biol. Chem. 267, 17864-17871, 1992

A:Title: Evidence for inserted sequences in the head region of nonmuscle myosin specific

myosin.

A:Reference number: A43402; MUID:92388144

A:Accession: B43402

A:Molecule type: mRNA

A:Residues: 1-2007 <TA>

A:Cross-references: GB:M93676; NID:g212448; PIDN:AAA48980.1; PID:g212452

A:Note: the sequence of residues 212-221 and 632-652 and the corresponding nucleotide se

A:Accession: A43402

A:Molecule type: mRNA

A:Residues: 1-211:222-631:653-2007 <TA>

A:Cross-references: GB:M93676; NID:g212448; PIDN:AAA48980.1; PID:g212449

A:Note: sequence extracted from NCBI backbone (NCBIN:112864)

C:Comment: Alternatively spliced segments 1 and 2 are found exclusively in nonmuscle myc

C:Superfamily: myosin heavy chain: myosin motor domain homology
C:Keywords: actin binding; alternative splicing; ATP; coiled coil; hydrolase; methyl a
F:1-2007/Product: myosin heavy chain-B, neuronal #status predicted <MYN>
F:1-211-222-631-653-2007/Product: myosin heavy chain-B, nonmuscle #status predicted <
F:88-802/Domain: myosin motor domain homology <AMOT>
F:178-185/Region: nucleotide-binding motif A (P-loop)
F:212-221/Region: alternatively spliced segment 1 #status experimental
F:559-593/Region: actin binding #status predicted
F:632-652/Region: alternatively spliced segment 2 #status experimental
F:692-714/Region: actin binding #status predicted
F:875-2007/Domain: coiled coil #status predicted <COI>
F:875-1315/Region: 52
F:1316-2007/Region: 196th meromyosin
F:129/Modified site: N6,N6-trimethyllysine (Lys) #status predicted
F:184/Binding site: ATP (Lys) #status predicted
F:732-742/Active site: Cys #status predicted
F:1954/Binding site: phosphate (Thr) (covalent) #status predicted
F:1987/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 14.6%; Score 157; DB 1; Length 2007;
Best Local Similarity 21.3%; Pred. No. 0.28;
Matches 65; Conservative 58; Mismatches 92; Indels 90; Gaps 10;

QY 4 INKLFPDLAQEEENV-----LDAEF--LKNELDSVKAQLSQK 38
Db 1109 IEELKIQDLAKKEBELQALARGDEAVQKNNALKVIRELOAQIAELQEDLESEKASRNKA 1168
QY 39 DREKRDQAIIITLRLTLEERNATVESLQNALNKAEMLCSTLK-----QMKFL 87
Db 1169 EKQKRDSELEALKTLEPTLDTTAAQELRTKREQEVALKKAIEETKRNHEAQIOEI 1228
QY 88 EQQR-----DETKQAREAHRLK-----CKKMTQDIFELLQSQK--- 122
Db 1229 QRHRAALEELSEQLQEQAKFKKANLEKKNQGLSDNKELCAYKVLQVQVRAESEHRRKRL 1288
QY 123 -SEVEEMIRMGVQSAVEDLAIVYCVSLKKEYN---LKEARKA----- 162
Db 1289 DAQVQELTAVTEGERLRVELAEKANKLQNELQVSSLSLEAEKKGKIFAKDAASLESQ 1348
QY 163 --TGLADRLKDLVSSRSKLTNTLNT---LDQAKLELSAQKDLQ---SADQETSLR 213
Db 1349 QDPQELLOEETROKLNLSRIROLEEKNMLQEQEEERARRNLEKOMLALOQLAEAK 1408
QY 214 KKSDD 218
Db 1409 KKVD 1413

RESULT 30
A27224
myosin heavy chain II - Acanthamoeba castellanii

N:Contains: myosin ATPase (EC 3.6.1.32)

C:Species: Acanthamoeba castellanii

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001

C:Accession: A27224

R:Hammer III, J.A.; Bowers, B.; Paterson, B.M.; Korn, E.D.
J. Cell Biol. 105, 913-925, 1987

A:Title: Complete nucleotide sequence and deduced polypeptide sequence of a nonmuscle

A:Reference number: A27224; MUID:87308395

A:Accession: A27224

A:Molecule type: DNA

A:Residues: 1-1509 <HAM>

A:Cross-references: GB:Y00624; GB:M12702; GB:M12703; GB:M19549; NID:g5585; PIDN:CAA68

C:Genetics:

A:Introns: 69/3; 119/3; 181/2

C:Superfamily: myosin heavy chain: myosin motor domain homology

C:Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleo

F:182-189/Region: nucleotide-binding motif A (P-loop)

F:344-376/Region: actin binding #status predicted

F:660-682/Region: actin binding #status predicted

F:848-1227/Domain: coiled coil #status predicted <COI>

F:1228-1247/Domain: hinge <HIN>
 F:148-1483/Domain: coiled coil #status predicted <CO>
 F:1483-1509/Domain: carboxyl-terminal <CBT>
 F:133/Modified site: N6, N6, N6-trimethyllysine (Lys) #status predicted
 F:188/Binding site: ATP (Lys) #status predicted

Query Match 14.6%; Score 156.5; DB 1; Length 1509;
 Best Local Similarity 20.9%; Pred. No. 0.22;
 Matches 59; Conservative 59; Mismatches 91; Indels 73; Gaps 7;

QY 10 DLAGEENVLD-----AEFLKNEIDSV-----KAQLS 36
 DB 1017 DALADANISSETLSKLNTERGADVDVNEIDVTATKLEKTKKSLSEELAOIRAOLE 1076
 QY 37 OKDEKEDSOAIIIDTLRDLTEERNATVESLONALNKAEMLCSTLKQKMFLEQODEKQ 96
 DB 1077 EEKSGKPAASSKAKQLOQLEDAESVDSLKSLSAEKSILTKAKDONRDLDEQLEDEBT 1136
 QY 97 AR-----EFAHRLKCKMKMTMEQIEELLQSQ-----RSEYEMIRDMGVGO----- 136
 DB 1137 VRANVDQKRALEKLELEQOVTALDOQKNAQAQKTLKTYDTRKRLLEAASAR 1196
 QY 137 -----SAVEQLAVYCVSLKKEYENLKEARRATGELADRLKDIY-----SSRSKLT 183
 DB 1197 LEKERKNALDEVAOLTDLDAERDSGAQORRKLNTRISELELENAPKTGASSEYK 1256
 QY 184 LNFELDOAKLELBSAQ-----KDLSADDEITSLRKSD 218
 DB 1257 LELGERLEELTLTAQPARAAERKNLUDKANLELELROEADD 1298

RESULT 31

S07537
 myosin heavy chain, smooth muscle, splice form 2 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1992 #sequence-revision 30-Jun-1992 #text-change 21-Jul-2000
 C:Accession: S07537; S10449
 R:Baby, P.; Perlasamy, M.
 J. Mol. Biol. 210, 673-679, 1989
 A:Title: Myosin heavy chain isoform diversity in smooth muscle is produced by different
 A:Reference number: S07537; MUID:50133920
 A:Accession: S07537
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-412 <BAB>
 A:Cross-references: EMBL:X16261
 A:Experimental source: Sprague-Dawley; smooth muscle; clone RAMHC15
 R:Baby, P.; Perlasamy, M.
 submitted to the EMBL Data Library, August 1989
 A:Reference number: S10449
 A:Accession: S10449
 A:Molecule type: mRNA
 A:Residues: 134-412 <BA2>
 A:Cross-references: EMBL:X16261; NID:956648; PIDN:CAA34347.1; PID:956649
 A:Experimental source: Sprague-Dawley; smooth muscle; clone RAMHC15
 C:Comment: For an alternate splice form see (PIR:S10450).
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: alternative splicing; ATP; cardiac muscle; heart; muscle

Query Match 14.5%; Score 156; DB 2; Length 412;
 Best Local Similarity 21.4%; Pred. No. 0.062;
 Matches 54; Conservative 55; Mismatches 95; Indels 48; Gaps 7;

QY 10 DLAGEENVLDLAEFLKNEIDSVKAQLSOK-----DREKDSQAIIDTLRDLTE 58
 DB 162 ELMQLOEDLAAERARQADLEKELEBELASSGNRLTODEKRLRLAIAQEELE 221
 QY 59 RNATVESLQNALNKAEMLCSTLKQKMFLEQODETKOAREAH----- 103
 DB 222 EOGNMEASDRVRKATLQADQLSNELVTERSQAOKNESARQOLERONKELSLQAEVGA 281

QY 104 LKCKMK-TMEQIEELLQSORSEVEEMIRDMGVGOSAVEQLAVYCVSLKKEYENLKEARKA 162
 DB 282 VKAKLKSTVALAEAKIYQLEEQIEQAEARK---QAATRLKQKQKXIKLEVLLQVEDERK- 337
 QY 163 TGEIADRLKQDLVSSRSKLTNTLTDQAKLE-----LRSQKQDSQADQ-----E 208
 DB 338 ---MVEQYKEQAEKGNTRVKQLKQLEAEESORINANRRKLQREIDEATESNEAMGRE 394
 QY 209 ITSILRKSDDEPP 220
 DB 395 VNALKSKLRGPP 406

RESULT 32

S60943
 RUD3 protein - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein O5028; protein YOR216c; protein YOR50-6
 C:Species: Saccharomyces cerevisiae
 C:Date: 15-Feb-1996 #sequence-revision 01-Mar-1996 #text-change 21-Jul-2000
 C:Accession: S60943; S67109; S71718
 R:Gallison, F.; Dujon, B.
 submitted to the EMBL Data Library, October 1995
 A:Description: Sequence and analysis of a 33 kb fragment from the right arm of chromo
 A:Reference number: S60938
 A:Accession: S60943
 A:Molecule type: DNA
 A:Residues: 1-484 <BOY>
 A:Cross-references: EMBL:X92441; NID:g1050762; PID:g1050768
 R:Boyer, J.; Fairhead, C.; Gallion, L.; Gallison, F.; Michaux, G.; Thierry, A.; Dujon
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S67104
 A:Accession: S67109
 A:Molecule type: DNA
 A:Residues: 1-484 <BOY>
 A:Cross-references: EMBL:Z75124; NID:g1420502; PID:e252397; PID:g1420503; MIPS:YOR216
 R:Gallison, F.; Dujon, B.
 yeast 12, 877-885, 1996
 A:Title: Sequence and analysis of a 33 kb fragment from the right arm of chromosome X
 A:Reference number: S71713; MUID:96437977
 A:Accession: S71718
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-484 <GAW>
 A:Cross-references: EMBL:X92441; NID:g1050762; PIDN:CAA63179.1; PID:g1050768
 C:Genetics:
 A:Gene: SGD:RUD3
 A:Cross-references: SGD:S0005742; MIPS:YOR216c
 A:Map position: 15R
 C:Function:
 A:Description: suppressor of usol-1 transport defect

Query Match 14.4%; Score 155; DB 2; Length 484;
 Best Local Similarity 24.3%; Pred. No. 0.083;
 Matches 51; Conservative 52; Mismatches 67; Indels 40; Gaps 8;

QY 24 LKNEIDSVKAQLSOKDREKDSQAIIDTLRDLTEERN---ATVESLONALNKAEMLCSTL 80
 DB 96 LREIERIKLELSHKKQDETPNEDFKNELANVIERDEFTQYDTLSISSMSKSIINKM 155
 QY 81 KKQKMFLEQODEKQAREAHRLKCKMKMTMEQIEELLQSORSEVEEMIRDMGVGOSAVE 140
 DB 156 KEAQKQLEVEQOELTE--YESQNLKLRK-----LEAKTENSEL-----OSTI- 197
 QY 141 QLAAYCVSLKKEYENLKEARKATGE-----LADRLKQDLVSSRSK-LKTLNTEL 188
 DB 198 -----VTLNTLELENLEKDEQSTEEVFLYESRTALEDE-KHDIIRKSKELNTYRK 250
 QY 189 DQAKLELRSQKQDSQADDEITSILRKSD 218
 DB 251 DQNLQVOELMILLENKKODISDLRTERDE 280

A>Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for residue
 C:Genetics:
 A:Gene: FlyBase:Mhc
 A:Cross-references: FlyBase:FBgn0002741
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: ATP

Query Match 14.4%; Score 154.5; DB 2; Length 1201;
 Best Local Similarity 22.8%; Pred. No. 0.22; Mismatches 91; Indels 53; Gaps 9;
 Matches 59; Conservative 56;

QY 10 DLAOEENVLDD-AEFLKNEIDSVKAQLSQDKREKRDQAIIIDTLRDTLEERNATVESLQ 67
 DB 903 DDAREQIGISERRANLQNELESRTLLEQADGRQAQELADAHQOLNEVSQAQNSIS 962
 QY 68 NALNKAMLCSTLKKQKFL---EQRQDETQAAREBAHRLCKMKMTQEIILLQSORS 123
 DB 963 AAKRKLESELQTLHSDLELNEAKNSEKAKKAMVDAARLADLRAEDQDAQTOEKLRK 1022
 QY 124 EVEEMIRDMGV-----GQSAVEQLAVYCVSLKKEYE-----NLKEAR 160
 DB 1023 ALRQQIKELQVRLDEAPANLKGKKAIOKLEQVRVRELENELDEQRRHADQKNLRKSE 1082
 QY 161 KATGELA-----DRLK---KDLVSS-RSKLKTINTLTDQAK-----LELRSAQKDLQ 203
 DB 1083 RRVKELSFQSEEDRKNNHERMODLVDRKQOKIKTKYKQIEEAEIAMLNLAKFRKAQOELE 1142
 QY 204 S-----ADQETSLRKK 215
 DB 1143 EAEERADLAEOAISKFRK 1161

RESULT 40

B35815
 myosin heavy chain 2, muscle - fruit fly (Drosophila melanogaster) (fragment)
 C:Species: Drosophila melanogaster
 C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 20-Jun-2000
 C:Accession: B35815
 R:Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
 Genes Dev. 4, 885-895, 1990
 A>Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion that
 A:Reference number: A35815; MUID:90346288
 A:Accession: B35815
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1201 <COIL>
 A:Cross-references: EMBL:X53155; NID:g8219; PIDN:CAA37311.1; PID:g2546939
 A>Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for residue
 C:Genetics:
 A:Gene: FlyBase:Mhc
 A:Cross-references: FlyBase:FBgn0002741
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: ATP

Query Match 14.4%; Score 154.5; DB 2; Length 1201;
 Best Local Similarity 22.8%; Pred. No. 0.22; Mismatches 91; Indels 53; Gaps 9;
 Matches 59; Conservative 56;

QY 10 DLAOEENVLDD-AEFLKNEIDSVKAQLSQDKREKRDQAIIIDTLRDTLEERNATVESLQ 67
 DB 903 DDAREQIGISERRANLQNELESRTLLEQADGRQAQELADAHQOLNEVSQAQNSIS 962
 QY 68 NALNKAMLCSTLKKQKFL---EQRQDETQAAREBAHRLCKMKMTQEIILLQSORS 123
 DB 963 AAKRKLESELQTLHSDLELNEAKNSEKAKKAMVDAARLADLRAEDQDAQTOEKLRK 1022
 QY 124 EVEEMIRDMGV-----GQSAVEQLAVYCVSLKKEYE-----NLKEAR 160
 DB 1023 ALRQQIKELQVRLDEAPANLKGKKAIOKLEQVRVRELENELDEQRRHADQKNLRKSE 1082
 QY 161 KATGELA-----DRLK---KDLVSS-RSKLKTINTLTDQAK-----LELRSAQKDLQ 203

DB 1083 RRVKELSFQSEEDRKNNHERMODLVDRKQOKIKTKYKQIEEAEIAMLNLAKFRKAQOELE 1142
 QY 204 S-----ADQETSLRKK 215
 DB 1143 EAEERADLAEOAISKFRK 1161

Search completed: September 4, 2002, 16:13:04
 Job time: 3248 sec

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